EG014US-Sequence Listing.txt Page

IAP20 Rec'd PCT/FTO 27 JAN 2006

SEQUENCE LISTING

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gat g Asp /																144	
gat d Asp /																192	
ggc g Gly / 65																240	
ttt g Phe /																288	
gat 1 Asp 1																336	
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tot a Ser 1																576	
gat g	gcc Ala	t t t Phe	gc t Ala	tat Tyr	gc t Ala	gtt Val	aaa Lys	aag Lys	cta Leu	gat Asp	acg Thr	aat Asn	gat Asp	ttc Phe	ttt Phe	624	

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Val Glu Pro Glu lle Trp Thr Leu Leu Asp Lys Val Arg Asp lle Al 210 gct gta tcg ggt gcg gaa atc ttg ccg gaa att cat gaa cac tat ac Ala Val Ser Gly Ala Glu lle Leu Pro Glu lle His Glu His Tyr Thr Ser Asp Tyr Tyr Val Tyr Asp Phe Al 225 att caa ttt aaa att gca gac cat gat tac tat gtt tat gat ttt gcl lle Gln Phe Lys lle Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Al 245 ctg cct atg gtg acg ctc tac agc cta tat tcg ggc aag gtt gac cc Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Ar 265 ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ct Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Le 280 gat aca cat gac ggt att ggt gtt gat gtt gat gtt agg gat atc ctg ac Asp Thr His Asp Gly lle Gly Val Val Asp Val Lys Asp Ile Leu Th 290 gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gc Asp Glu Glu lle Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Al 330 aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat at Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Il 325 tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat gat gat gat gat gat g	1			195					200					205				
At a Val Ser Gly Ala Glu IIe Leu Pro Glu IIe His Glu His Tyr Th 230 att caa ttt aaa att gca gac cat gat tac tat gtt tat gat ttt glie Gin Phe Lys IIe Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Al 245 ctg cct atg gtg acg ctc tac agc cta tat tcg ggc aag gtt gac cg Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Ar. 265 ctt gcc aaa tgg ctg aaa atg agt ccg atg aaa cag ttc acc acc ct Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Ar. 285 gat aca cat gac ggt att ggt gtg gtt gat gt gaag gat atc ctg ac Asp Thr His Asp Gly IIe Gly Val Val Asp Val Lys Asp IIe Leu Th 295 gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gc Asp Glu Glu IIe Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Al 315 aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat at Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp II 325 tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat ca Tyr Gin IIe Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gli 345 cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ct gat gc Lys Tyr Phe Leu Ala Arg Leu IIe Gln Ala Phe Ala Pro Gly IIe Pr. 355 cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ct gat gat gat ca Tyr Gln IIe Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Leu Glu Val Tyr Tyr Val Gly Arg Asn IIe Asn Arg His Tyr Tyr Ser Glu Glu IIe Ala Lys Glu Val Lys And Ala Arg His Tyr Tyr Ser Ala Leu Asn Arg His Tyr Tyr Ser Glu Glu IIe Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu And Chy Glu Val Lys Ala Leu And Leu Asn Leu Asp Leu Ash Chy Glu Val Lys Arg Pro Val Val Lys Ala Leu And Chy Glu Val Lys Arg Pro Val Val Lys Ala Leu And Chy Arg IIe Glu Val Glu Thr Pro Asn Glu Ala Thr IIe Val IIe Gli Ala Gly Arg IIe Glu Val Glu Thr Pro Asn Glu Ala Thr IIe Val IIe Gli Ala Gly Arg IIe Glu Val Glu Thr Pro Asn Glu Ala Thr IIe Val IIe Gli Gly Arg IIe Glu Val Glu Thr Pro Asn Glu Ala Thr IIe Val IIe Gli Gly Arg IIe Glu Val Glu Thr Pro Asn Glu Ala Thr IIe Val IIe Gli Gly Arg IIe Glu Val Glu Thr Pro Asn Glu Ala Thr IIe Val IIe Gl	Val Glu P	al G	Glu	cct Pro	gaa Glu	atc	tgg Trp	Thr	ctg Leu	cta Leu	ga t Asp	aaa Lys	Val	cgt Arg	ga t Asp	ata Ile	gct Ala	672
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Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Ar. 260 ctt gcc aaa tgg ctg aaa atg acg ccg atg aaa cag ttc acc acc ct Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe Thr Thr Leu 285 gat aca cat gac ggt att ggt gtg gtt gat gtt aag gat atc ctg ac Asp Thr His Asp Gly lie Gly Val Val Asp Val Lys Asp lie Leu Th 290 gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gc Asp Glu Glu lie Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Al 315 aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat at Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp li 325 tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat ca Tyr Gln lie Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gli 340 aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cc Lys Tyr Phe Leu Ala Arg Leu lie Gln Ala Phe Ala Pro Gly lie Pro 360 cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tt Glu Val Tyr Tyr Val Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser Glu Glu Ser Thr Lys Glu Gly Arg Asn lie Asn Arg His Tyr Tyr Ser Glu Glu Ser Thr Lys Glu Gly Arg Asn lie Asn Arg His Tyr Tyr Ser Glu Glu lie Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu Ala Clu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu Ala Clu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu Ala Clu Arg Ile Glu Val Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp Leu Arg Clu Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Arg Glu Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Arg Glu Arg Ile Glu Val Ile Clu Arg Glu Arg Ile Glu Val Ile Clu Arg Glu Arg Ile Glu Val Ile Clu Arg Glu Arg Ile Glu Val Ile Gli Arg Ile Glu Val Ile Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Gli Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Gli Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Gli Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Gli Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Gli Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Gli Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Gli Thr Pro Asn Glu Ala Thr Ile Val Ile Gli Gli Thr Pro Asn Glu Ala Thr Ile Val Ile Gli G	att caa t ile Gin P	itt c	caa Gin	ttt Phe	aaa Lys	Пe	gca Ala	gac Asp	cat His	gat Asp	Туг	tat Tyr	gtt Val	tat Tyr	gat Asp	Phe	gcc Ala	768
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Asp Thr His Asp Gly lie Gly Val Val Asp Val Lys Asp lie Leu Th 290 gac gaa gaa att acc tat act tct aat gag ctt tat aag gtc ggt gc Asp Glu Glu lie Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Al: 315 aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat at Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp li: 325 tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat gat ca. Tyr Gln lie Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gl: 340 aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cc. Lys Tyr Phe Leu Ala Arg Leu lie Gln Ala Phe Ala Pro Gly lie Pro 355 cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tt. Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Lei 370 ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat ag Leu Glu Ser Thr Lys Glu Gly Arg Asn lie Asn Arg His Tyr Tyr Se 390 agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ct Ser Glu Glu lie Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu 405 tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg ga ttg gac gcc gt att gat gat gat gac gcc gcc att gtc aag gca ct gcc aat atc gcc gcc att gtc aag gca ct gcc aat atc gcc gcc att gtc aag gca ct gcc aat atc gcc gcc att gtc aag gca ct gcc aat atc gcc gcc att gtc aag gca ct gcc aat atc gcc gcc att gtc aag gca ct gcc aat atc gcc gcc att gtc aag gca ct gcc aat atc gcc gcc att gtc aag gca ct gcc aat acg cat att gcc aat gcc gcc att gtc aag gca ct gcc aat acgc gcc acc att gcc aat gcc gcc att gcc aat gcc acc acc gcc acc acc gcc acc acc gcc acc a	Leu Ala L	tt g .eu A	ı Ala	Lys	tgg Trp	ctg Leu	aaa Lys	atg Met	Ser	ccg Pro	atg Met	aaa Lys	cag Gln	Phe	acc Thr	acc Thr	ctt Leu	864
Asp Glu Glu Ile Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Alt 305 aat gtc aat cgt aag tat tca act gcc gaa tat aat aac ttg gat at Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Il 325 tat caa att aat tca act tac tat tca gca ctt ggt gat gat gat ca Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gl 340 aaa tac ttt ttg gcc cgc ttg ata caa gct ttt gct cca ggt att cc Lys Tyr Phe Leu Ala Arg Leu Ile Gln Ala Phe Ala Pro Gly Ile Pro 355 cag gtt tat tac gtt ggc ttt tta gct ggc aag aat gat ctt gaa tt Gln Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Lei 370 ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat ag Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Ser 390 agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ct Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Lei 405 tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg ga ggc cgt att gaa gca ct aat cag tca gca gct ttt gat ttg ga ggc cgt att gaa gtg gaa ggc cgt att gaa gca ct ggc ca gct att gat gat ggc cgt att gaa gca ct ggc cag gca cat gca gca ct gca att gca gca gca ct gca gca ct gca aat gaa gca ct gca gca ct gca aat gaa gca ct gca gca ct gca aat gaa gca ct gca aat gaa gca gca ca aat gaa gca ca aat gaa gca gca ca aat gaa gca gca ca aat gaa gca ca aat gaa gca gca ca aat gaa gca gca act att gca aat gca gca ca aat gaa gca gca aat gaa gca gca ca aat gaa gca gca ca aat gaa gca gca act aat gaa gc	Asp Thr H	\sp T	Thr	cat His	gac Asp	ggt Gly	att He	Gly	gtg Val	gtt Val	gat Asp	gtt Val	Lys	gat Asp	atc Ile	c t g Leu	act Thr	912
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Lys Tyr Phe Leu Ala Arg Leu Ile Gin Ala Phe Ala Pro Gly Ile Pro 355 cag git tat tac git ggc tit ta gct ggc aag aat gat cit gaa tit Gin Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu 370 ctg gaa agc act aaa gaa ggc cgc aat atc aac cgt cat tat tat ag Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His Tyr Tyr Se 385 agt gaa gaa att gct aag gaa gtg aag cgg cca git gtc aag gca ct Ser Glu Glu Ile Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu 405 tta aat ctc tit act tac cgc aat cag tca gca gct tit gat tig ga Leu Asn Leu Phe Thr Tyr Arg Asn Gin Ser Ala Ala Phe Asp Leu Asg Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu Val Ile Glu Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu					Asn					Ser					Asp			1056
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Leu Glu Ser Thr Lys Glu Gly Arg Asn lie Asn Arg His Tyr Tyr Se 385 agt gaa gaa att gct aag gaa gtg aag cgg cca gtt gtc aag gca ct Ser Glu Glu lie Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu 405 tta aat ctc ttt act tac cgc aat cag tca gca gct ttt gat ttg ga Leu Asn Leu Phe Thr Tyr Arg Asn Gln Ser Ala Ala Phe Asp Leu Asp 420 ggc cgt att gaa gtg gaa acg cca aat gaa gcg acc att gtc ata ga Gly Arg lie Glu Val Glu Thr Pro Asn Glu Ala Thr lie Val lie Glu	Gin Val T	31n V	ı Val	tat Tyr	tac Tyr	gtt Val	ggc Gly	Phe	tta Leu	gct Ala	ggc Gly	aag Lys	Asn	gat Asp	ctt Leu	gaa Glu	tta Leu	1152
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<210> 2 <211> 481 <212> PRT <213> Streptococcus mutans

EG014US-Sequence Listing.txt Page

Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn lie Glu Asn Tyr Phe Gly $20 \hspace{1cm} 25 \hspace{1cm} 30$

Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45

Asp Arg Gly Phe Ala Pro IIe Asp Tyr His Glu Val Asp Ser Ala Phe 50 55 60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met 11e Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys $85 \hspace{0.25cm} 90 \hspace{0.25cm} 95$

Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu 100 105 110

Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gin Giu Asp Val 115 120 125

Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gin Giu lie Gin 130 140

Phe Ala Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu 145 150 155 160

Gin lie Asp Leu Asp Val Thr Lys Giu Val Thr Met Asp Phe lie Arg 165 170 175

Ser Thr lie Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu lie Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

Val Glu Pro Glu Ile Trp Thr Leu Leu Asp Lys Val Arg Asp Ile Ala 210 215 220

Ala Val Ser Gly Ala Glu IIe Leu Pro Glu IIe His Glu His Tyr Thr 225 230 235 240

lle Gln Phe Lys lle Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg 260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly IIe Gly Val Val Asp Val Lys Asp IIe Leu Thr 290 295 300

Asp Glu Glu lle Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala 305 310 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile 325 330 335

Tyr Gin lie Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Gin 340 350

EG014US-Sequence Listing.txt Lys Tyr Phe Leu Ala Arg Leu IIe Gin Ala Phe Ala Pro Gly IIe Pro 355 360 365 GIn Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu 370 375 380 Leu Glu Ser Thr Lys Glu Gly Arg Asn IIe Asn Arg His Tyr Tyr Ser 385 390 395 400 Ser Glu Glu IIe Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu 405 410 415 Leu Asn Leu Phe Thr Tyr Arg Asn Gin Ser Ala Ala Phe Asp Leu Asp 420 425 430 Gly Arg lie Glu Val Glu Thr Pro Asn Glu Ala Thr lie Val lie Glu
435 440 445 Arg Gin Asn Lys Asp Gly Ser His IIe Ala Thr Ala Glu IIe Asn Leu 450 455 460 Gin Asp Met Thr Tyr Arg Val Thr Giu Asn Asp Gin Thr Ile Ser Phe 465 470 475 480 <210> 3 <211> 1434 <212> DNA <213> Strep Streptococcus pneumoniae <220> <221> CDS <222> (1)..(1434) atg cca att caa aat aaa acc atg ttg att acc tat tct gat agc ctt Met Pro lle Gin Asn Lys Thr Met Leu lle Thr Tyr Ser Asp Ser Leu 1 5 10 15

96 gga aat aat ctt aaa gac tta tat gat aat ttg gaa gag cat ttt gga Gly Asn Asn Leu Lys Asp Leu Tyr Asp Asn Leu Glu Glu His Phe Gly 20 25 30 gat gct att gga gga gtt cac ctt tta cca ttt ttc cca tca aca gtt Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Val 35 40 45 144 gat cgt gga ttt gcg cca gtt gac tac gac gaa gtg gac tca gct ttt Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe 50 55 ggt gat tgg gag gat gtg aag cgt tta ggt gag aaa tat tat ctt atg Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 80 240 ttt gat ttt atg att aat cat att tct cgt caa tcc aag tat tat aag Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95 gac tat caa gaa aaa cat gaa gcc agt gaa ttt aaa gct ctc ttt tta Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Ala Leu Phe Leu 100 105 110 336 aac tgg gat aag ttt tgg cca gaa aac cgt ccg aca cag tct gat gta Asn Trp Asp Lys Phe Trp Pro Glu Asn Arg Pro Thr Gln Ser Asp Val 115 120 125 384 432 gat tta att tac aag cgt aag gat cgt gca cca aag caa gag att gtg Asp Leu lle Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gin Glu lle Vali 130 135 140 ttt gaa gat ggt tca gtg gaa cat ttg tgg aat acc ttt ggt gag gag Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu 480

EG014US-Sequence Li	sting.txt	Page 5			
145	150	15	5	160	
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aag acc att cag cac Lys Thr IIe GIn His 180					
gat gcc ttt gct tat Asp Ala Phe Ala Tyr 195					
gtg gaa cca gat att Val Glu Pro Asp Ile 210					
gct gag tat ggg aca Ala Glu Tyr Gly Thr 225			e His Glu His		
att cag ttt aaa ata lle Gin Phe Lys lie 245	· Āla Āsp His		r Val Tyr Asp		
ctt cca atg gtg aca Leu Pro Met Val Thr 260	ctt tat act Leu Tyr Thr	ctt tac ag Leu Tyr Sea 265	t tcc aga aca r Ser Arg Thr 270	gag cgt 816 Glu Arg	
ttg gct aag tgg tta Leu Ala Lys Trp Leu 275					
gat acc cat gat ggg Asp Thr His Asp Gly 290	att gga gta lle Gly Val 295	gta gat gte Val Asp Val	c aag gat atc I Lys Asp lie 300	ctg acc 912 Leu Thr	
gat gag gag att gad Asp Glu Glu Ile Asp 305	tat gct tca Tyr Ala Ser 310	aat gaa cte Asn Glu Let 31!	u Tyr Lys Val	gga gcc 960 Gly Ala 320	
aat gtc aaa cgt aag Asn Val Lys Arg Lys 325	Tyr Ser Ser	gcc gag ta Ala Glu Tyi 330	r Asn Asn Leu .	gat atc 1008 Asp lle 335	
tac caa atc aat tca Tyr Gin ile Asn Ser 340					
aag tat tit cic gct Lys Tyr Phe Leu Ala 355					
cag att tac tat gtg Gin lie Tyr Tyr Vai 370					
tta gaa gaa act aaa Leu Glu Glu Thr Lys 385	gaa ggt cga Glu Gly Arg 390	aat att aat Asn lle Asr 395	n Arg His Tyr	tat agc 1200 Tyr Ser 400	
aac gag gaa ata gca Asn Glu Glu Ile Ala 405	Lys Glu Val	caa cga cci GIn Arg Pro 410	o Val Val Lys .	gcc ctt 1248 Ala Leu 415	
ctc aat cta tit tct Leu Asn Leu Phe Ser 420	ttc cgt aac Phe Arg Asn	cgt tca gaa Arg Ser Glu 425	a gcc ttt gat u Ala Phe Asp 430	cta gaa 1296 Leu Glu	
ggg act act gag ata Gly Thr Thr Glu lle 435	gag aca cca Glu Thr Pro 440	aca gct cat Thr Ala His	c agc att gta s Ser lle Val 445	atcaaa 1344 lle Lys	
cgt caa aat aaa gat Arg Gin Asn: Lys Asg 450	aag too gta Lys Ser Val 455	aca gca gta Thr Ala Val	a gta gaa att 1 Val Glu lle 460	gat ttg 1392 Asp Leu	
caa aat cag act tat Gin Asn Gin Thr Tyr 465			y Val Glu Val	1434	

EG014US-Sequence Listing.txt

<212> PRT
<213> Streptococcus pneumoniae

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Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe 50 60

Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met IIe Asn His IIe Ser Arg Gin Ser Lys Tyr Tyr Lys 85 90 95

Asp Tyr Gln Glu Lys His Glu Ala Ser Glu Phe Lys Ala Leu Phe Leu 100 105 110

Asn Trp Asp Lys Phe Trp Pro Giu Asn Arg Pro Thr Gin Ser Asp Val

Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gin Glu lie Val

Phe Glu Asp Gly Ser Val Glu His Leu Trp Asn Thr Phe Gly Glu Glu 145 150 155 160

Gin ile Asp Leu Asp Val Thr Lys Giu Val Thr Met Giu Phe ile Arg 165 170 175

Lys Thr lie Gin His Leu Ala Ser Asn Gly Cys Asp Leu lie Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

Val Glu Pro Asp lle Trp Asp Leu Leu Asp Lys Val Arg Asp lle Ala 210 215 220

Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu lle His Glu His Tyr Ser 225 230 235 240

lle Gin Phe Lys lle Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg 260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly IIe Gly Val Val Asp Val Lys Asp IIe Leu Thr 290 295 300

Asp Glu Glu lle Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala 305 310 320

EG014US-Sequence Listing.txt Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp Ile 325 330 335 Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Val 340 345 350 Lys Tyr Phe Leu Ala Arg Leu Ile Gin Ala Phe Ala Pro Gly Ile Pro 355 360 365 GIn lie Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu 370 375 380 Leu Glu Glu Thr Lys Glu Gly Arg Asn 11e Asn Arg His Tyr Tyr Ser 385 390 395 400 Asn Giu Giu ile Ala Lys Giu Val Gin Arg Pro Val Val Lys Ala Leu 405 410 415 Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Glu Ala Phe Asp Leu Glu 420 425 430 Gly Thr Thr Glu lie Glu Thr Pro Thr Ala His Ser lie Val lie Lys 435 440 445 Arg Gin Asn Lys Asp Lys Ser Vai Thr Ala Val Val Glu ile Asp Leu 450 460 Gin Asn Gin Thr Tyr Arg Val Ile Giu Asn Giy Val Giu Val 465 470 475 <210> 5 <211> 1443 <212> DNA <213> Streptococcus sorbinus <220>
<221> CDS
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gat tta att tat aaa cgt aaa gac aag gct cct atg cag gag att gtc Asp Leu lie Tyr Lys Arg Lys Asp Lys Ala Pro Met Gin Giu lie Val 432

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caa att gat c Gin lie Asp L	cta gat gtt ac Leu Asp Val Th 165	r Lys Glu V	gtg acc atg Vai Thr Met 170	Asp Phe	atc aaa lle Lys 175	528
Lys Asn Ile C	gag cat cta go Glu His Leu Al 180					576
gat gcc ttt g Asp Ala Phe A 195	gcc tac gcc gt Ala Tyr Ala Va	g aaa aaa t I Lys Lys L 200	ttg gac act eu Asp Thr	aat gat Asn Asp 205	ttc ttt Phe Phe	624
gtc gaa cca g Val Glu Pro 0 210	gaa att tgg ga Glu lle Trp As 21	p Leu Leu T	icc aag gta Thr Lys Val 220	cag aca Gin Thr	atc gcc lle Ala	672
	ggg gca gat at Gly Ala Asp li 230					720
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	tgg ctg gct aa Trp Leu Ala Ly					864
	gat ggc att gg Asp Gly lle Gl 29	y Val Val A		Asp ile		912
	att gct tac ac lle Ala Tyr Th 310					960
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Tyr Gin ile A	aac tog acc ta Asn Ser Thr Ty 340	c tat tca g r Tyr Ser A 345	gcc ctt ggt Ala Leu Gly	gac gat Asp Asp 350	gac aag Asp Lys	1056
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caa gtt tat t GIn Va! Tyr T 370	tat git gga ci Tyr Val Gly Le 37	u Leu Ala G	gga aaa aac Gly Lys Asn 380	gat ctg Asp Leu	aag ctc Lys Leu	1152
ttg gaa aaa a Leu Glu Lys T 385	acc aag gaa gg Thr Lys Glu Gi 390	t cgc aat a y Arg Asn I	atc aat cgt lle Asn Arg 395	cat tat His Tyr	tat agc Tyr Ser 400	1200
agt gaa gag a Ser Glu Glu I	att gct cac ga Ile Ala His Gi 405	u Val Glu A	egg cca gtt Arg Pro Val 110	Val Lys	gct ttg Ala Leu 415	1248
lle Lys Leu P	ttt agc tat cg Phe Ser Tyr Ar 420	c aac aac t g Asn Asn S 425	tet caa get Ser Gin Ala	ttc gac Phe Asp 430	tta gac Leu Asp	1296
ggc agc ctt g Gly Ser Leu 0 435	gaa acg gaa gt Glu Thr Glu Va	t ctg gat g I Leu Asp A 440	gac cac acc Asp His Thr	atc gtt lle Val 445	atc aag lle Lys	1344
cgt tct aat c Arg Ser Asn 0 450	cag gac aag ag Gin Asp Lys Se 45	r Ala Leu A	ct caa gct Na Gin Ala 460	Val lie	aat ttg Asn Leu	1392
	acc tat cag gt Thr Tyr Gin Va 470					1440

gaa Glu

> <210> 6 <211> 481

(212) PRI (213) Streptococcus sorbinus

<400> 6

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Gly Arg Asn Leu Lys Glu Leu Asp Glu Asn lie Ser Ile Tyr Phe Gly 20 25 30

Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45

Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Lys Val Asp Pro Ala Phe 50 55 60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Ala Lys Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met lie Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95

Asp Phe Gin Glu Lys Lys Asp Ala Ser Asp Tyr Ala Asp Leu Phe Leu 100 105 110

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Asp Leu lie Tyr Lys Arg Lys Asp Lys Ala Pro Met Gin Giu lie Val 130 135 140

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Gin ile Asp Leu Asp Val Thr Lys Giu Vai Thr Met Asp Phe ile Lys 165 170 175

Lys Asn Ile Glu His Leu Ala Val Asn Gly Cys Asp Leu Ile Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Ash Asp Phe Phe 195 200 205

Val Glu Pro Glu Ile Trp Asp Leu Leu Thr Lys Val Gln Thr Ile Ala 210 215 220

Lys Glu Ala Gly Ala Asp Ile Leu Pro Glu Ile His Glu His Tyr Ser 225 230 235 240

lle Gin Phe Lys Ile Ala Giu His Asp Tyr Phe lle Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Arg Val Gin Arg 260 270

Leu Ala Asp Trp Leu Ala Lys Ser Pro Met Lys Gln Phe Thr Thr Leu 275 280 285

EG014US-Sequence Listing.txt

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Asp Glu Glu IIe Ala Tyr Thr Ser Asp Gln Leu Tyr Lys Val Gly Ala 305 310 315 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp Ile 325 330 335

Tyr Gin lie Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Asp Lys 340 345 350

Lys Tyr Phe Leu Ala Arg Leu Ile Gin Ala Phe Ala Pro Giy Ile Pro 355 360 365

Gin Vai Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp Leu Lys Leu 370 375 380

Leu Glu Lys Thr Lys Glu Gly Arg Asn IIe Asn Arg His Tyr Tyr Ser 385 390 395 400

Ser Glu Glu lle Ala His Glu Val Glu Arg Pro Val Val Lys Ala Leu 405 410 415

lle Lys Leu Phe Ser Tyr Arg Asn Asn Ser Gin Ala Phe Asp Leu Asp 420 430

Gly Ser Leu Glu Thr Glu Val Leu Asp Asp His Thr !le Val !le Lys 435 440 445

Arg Ser Asn Gln Asp Lys Ser Ala Leu Ala Gln Ala Val IIe Asn Leu 450 460

Gin Asp Leu Thr Tyr Gin Val Thr Giu Asn Giy Gin Thr lie Thr Phe 465 470 475 480

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<210> 7 <211> 1470 <212> DNA <213> Leuconostoc mesenteroides

<220> <221> CDS <222> (1)..(1470)

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ggc aaa aac tta aaa gat gtt cat caa gtc ttg aaa gaa gat att gga Gly Lys Asn Leu Lys Asp Val His Gln Val Leu Lys Glu Asp 11e Gly 20 25 30

gat gcg att ggt ggg gtt cat ttg ttg cct ttc ttc cct tca aca ggt Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45144

gat cgc ggt ttt gcg cca gcc gat tat act cgt gtt gat gcc gca ttt Asp Arg Gly Phe Ala Pro Ala Asp Tyr Thr Arg Val Asp Ala Ala Phe 50 55 60 192

ggt gat tgg gca gat gtc gaa gca ttg ggt gaa gaa tac tat ttg atg Gly Asp Trp Ala Asp Val Glu Ala Leu Gly Glu Glu Tyr Tyr Leu Met 65 70 80

ttt gac ttc atg att aac cat att tct cgt gaa tca gtg atg tat caa Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Val Met Tyr Gln 288

EG0	14US-	-Seqi	Jenc (e Li:	sting	g. tx	t	Pag	ge 11	I						
				85					90					95		
gat Asp	ttt Phe	aag Lys	aag Lys 100	aa t As n	cat His	gac Asp	gat Asp	tca Ser 105	aag Lys	tat Tyr	aaa Lys	gat Asp	ttc Phe 110	ttt Phe	at t ile	336
cgt Arg	tgg Trp	gaa Glu 115	aag Lys	ttc Phe	tgg Trp	gca Ala	aag Lys 120	gcc Ala	ggc Gly	gaa Glu	aac Asn	cgt Arg 125	cca Pro	aca Thr	caa Gin	384
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ggt Gly	gaa Glu	gaa Glu	caa Gln	att ile 165	gac Asp	att	gat Asp	gtt Val	aat Asn 170	tca Ser	gcc Ala	att	gcc Ala	aag Lys 175	gaa Glu	528
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					cca Pro											672
					tta Leu 230											720
					aaa Lys											768
					atg Met											816
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att 11e 305	cta Leu	act Thr	ga t Asp	ga t Asp	gaa Glu 310	att	gac Asp	tac Tyr	gct Ala	tct Ser 315	gaa Glu	caa Gin	c t t Leu	tac Tyr	aag Lys 320	960
gtt Val	ggc Gly	gcg Ala	aa t As n	gtc Val 325	aaa Lys	aag Lys	aca Thr	tat Tyr	tca Ser 330	tct Ser	gc t Ala	tca Ser	tac Tyr	aac Asn 335	aac Asn	1008
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gat Asp	ga t Asp	gca Ala 355	gca Ala	tac Tyr	t t g Leu	t t g Leu	agt Ser 360	cgt Arg	gtc Val	t t c Phe	caa Gln	gtc Val 365	ttt Phe	gcg Ala	cct Pro	1104
gga Gly	att He 370	cca Pro	caa Gln	att	tat Tyr	tac Tyr 375	gtt Val	ggt Gly	ttg Leu	t t g Leu	gca Ala 380	gg t Gly	gaa Glu	aac Asn	ga t Asp	1152
atc lie 385	gcg Ala	ctt Leu	t t g Leu	gag Glu	tca Ser 390	act Thr	aaa Lys	gaa Glu	gg t Gly	cgt Arg 395	aa t As n	att	aac Asn	cgt Arg	cat His 400	1200
Tyr	Tyr	Thr	Arg	GI u 405	gaa Glu	Va I [.]	Lys	Ser	410	Val	Lys	Arg	Pro	Val 415	Va I:	1248
gc t Ala	aac Asn	tta Leu	ttg Leu 420	aag Lys	cta Leu	t t g Leu	tca Ser	tgg Trp 425	cgt Arg	aat Asn	gaa Glu	agc Ser	cct Pro 430	gca	ttt Phe	1296

EG014US-Sequence Listing.txt

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<210> 8 <211> 490 <212> PRT <213> Leuconostoc mesenteroides

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Gly Lys Asn Leu Lys Asp Val His Gln Val Leu Lys Glu Asp lle Gly 25 30

Asp Ala IIe Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly $35 \hspace{1cm} 40 \hspace{1cm} 45$

Asp Arg Gly Phe Ala Pro Ala Asp Tyr Thr Arg Val Asp Ala Ala Phe 50 55 60

Gly Asp Trp Ala Asp Val Glu Ala Leu Gly Glu Glu Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met IIe Asn His IIe Ser Arg Glu Ser Val Met Tyr Gln 85 90 95

Asp Phe Lys Lys Asn His Asp Asp Ser Lys Tyr Lys Asp Phe Phe 11e 100 105 110

Arg Trp Glu Lys Phe Trp Ala Lys Ala Gly Glu Asn Arg Pro Thr Gln $115\,$ $120\,$ $125\,$

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Glu lie Thr Phe Asp Asp Gly Thr Thr Glu Asn Leu Trp Asn Thr Phe 145 150 155 160

Gly Glu Glu Gln lle Asp lle Asp Val Asn Ser Ala lle Ala Lys Glu 165 170 175

Phe lie Lys Thr Thr Leu Glu Asp Met Val Lys His Gly Ala Asn Leu 180 185 190

lie Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Asp Thr Asn 195 200 205

Asp Phe Phe Val Glu Pro Glu lle Trp Asp Thr Leu Asn Glu Val Arg 210 215 220

Glu lle Leu Thr Pro Leu Lys Ala Glu lle Leu Pro Glu lle His Glu 225 230 240

EG014US-Sequence Listing.txt His Tyr Ser lle Pro Lys Lys lle Asn Asp His Gly Tyr Phe Thr Tyr 245 250 255

Asp Phe Ala Leu Pro Met Thr Thr Leu Tyr Thr Leu Tyr Ser Gly Lys 260 265 270

Thr Asn Gin Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe 275 280 285

Thr Thr Leu Asp Thr His Asp Gly IIe Gly Val Val Asp Ala Arg Asp 290 295 300

lle Leu Thr Asp Asp Glu lle Asp Tyr Ala Ser Glu Gin Leu Tyr Lys 305 310 315 320

Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ser Tyr Asn Asn 325 330 335

Leu Asp ile Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn 340 350

Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gin Val Phe Ala Pro 355 360 365

Gly lie Pro Gin lie Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp 370 375 380

lle Ala Leu Leu Glu Ser Thr Lys Glu Gly Arg Asn lle Asn Arg His 385 390 395

Tyr Tyr Thr Arg Glu Glu Val Lys Ser Glu Val Lys Arg Pro Val Val 405 410 415

Ala Asn Leu Leu Lys Leu Leu Ser Trp Arg Asn Glu Ser Pro Ala Phe 420 425 . 430

Asp Leu Ala Gly Ser lie Thr Val Asp Thr Pro Thr Asp Thr Thr lie 435 440 445

Val Val Thr Arg Gin Asp Giu Asn Giy Gin Asn Lys Ala Val Leu Thr 450 455 460

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Val Met Ser Ser Asp Asn Leu Thr Gln Asn 485 490

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<220>
<221> CDS
<222> (1).. (1467)

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gac gcg att ggt gga gtt cat ctg ctg cct ttt ttt ccg tca acc gga Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly

EGUI	405-	Sequ	rence	LIS	ting	. IXI		гав	e 14	•						
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cgt Arg	tgg Trp	gaa Glu 115	aag Lys	ttc Phe	tgg Trp	ccg Pro	aaa Lys 120	gga Gly	cgc Arg	ccg Pro	acg Thr	aag Lys 125	gcc Ala	ga t As p	atc lle	384
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Leu	Ala	Lys 275		Leu	Lys	Met	Ser 280	Pro	Lys	Lys	GIn	285	Thr	Thr	Leu	864
Asp	1hr 290	His	ga t Asp	Gly	116	G19 295	Val	vai	ASD	АІА	300	ASD	116	Leu	LAF	912
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EGU 1	405-	-2edr	ence	E E I S	gniji	ζ. ιχι		ган	e 15	•						
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cga Arg	act Thr 450	tca Ser	acc Thr	aat Asn	ggc Gly	caa Gln 455	gac Asp	acc Thr	gcg Ala	gaa Glu	tta Leu 460	acc Thr	gct Ala	aa t As n	gtg Val	1392
gct Ala 465	cta Leu	aaa Lys	acc Thr	ttt Phe	act Thr 470	ata ile	aag Lys	gaa Glu	aat Asn	gat Asp 475	aaa Lys	att lie	att	tta Leu	att 11e 480	1440
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Gly	Lys	Asn	11e 20	Lys	Glu	Leu	GIn	Tyr 25	He	Leu	Asp	Lys	Tyr 30	11e	Gly	
Asp	Ala	11e 35	Gly	Gly	Val	His	Leu 40	Leu	Pro	Phe	Phe	Pro 45	Ser	Thr	Gly	
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	130			Lys		135					140					
145				Ser	150					155					160	
				Asn 165					170					175		
Asp	Thr	Leu	GI n 180	Ser	Met	Val	Lys	His 185		Ala	Asp	Leu	11e 190	Arg	Leu	

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Leu Ala Lys Trp Leu Lys Met Ser Pro Lys Lys Gin Phe Thr Thr Leu 275 280 285

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Asn Val Lys Arg Thr Tyr Ser Ser Ala Ala Tyr Asn Asn Leu Asp lle 325 330 335

Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys 340 345 350

Gin lie Tyr Tyr Ala Giy Leu Leu Ala Giy Giu Asn Asp Leu Asp Leu 370 380

Leu Glu Lys Thr Lys Glu Gly Arg Asn Ite Asn Arg His Tyr Tyr Ser 385 390 395

Giu Giu Vai Ala Aśn Glu Vai Gin Arg Pro 11e Vai Ala Cys Leu 405 410 415

Leu Lys Leu Ala Trp Arg Asn Arg Ser Ala Ala Phe Asp Leu Gin 420 425 430

Gły Asp ile Gin Val Ser Ala Thr Asp Lys Asn Glu ile Lys Ile Ile 435 440 445

Arg Thr Ser Thr Asn Gly Gln Asp Thr Ala Glu Leu Thr Ala Asn Val 450 460

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gat Asp	tta Leu 130	att	tac Tyr	aag Lys	cgt Arg	aag Lys 135	gat Asp	cgt Arg	gca Ala	cca Pro	aag Lys 140	caa Gin	gag Glu	att He	gtt Val	432
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Asp Arg Gly Phe Ala Pro Val Asp Tyr Asp Glu Val Asp Ser Ala Phe 50 55 60

Gly Asp Trp Glu Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80

Phe Asp Phe Met 11e Asn His 11e Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95

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Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Lys Gin Glu lie Val 130 135 140

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Gln lle Asp Leu Asp Val Thr Lys Glu Val Thr Met Glu Phe lle Arg 165 170 175

Lys Thr lle Gln His Leu Ala Ser Asn Gly Cys Asp Leu lle Arg Leu 180 185 190

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Val Glu Pro Asp lle Trp Asp Leu Leu Asp Lys Val Arg Asp lle Ala 210 215 220

Ala Glu Tyr Gly Thr Glu Leu Leu Pro Glu lle His Glu His Tyr Ser 225 230 235 240

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Leu Pro Met Val Thr Leu Tyr Thr Leu Tyr Ser Ser Arg Thr Glu Arg 260 270

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Asp Glu Glu lle Asp Tyr Ala Ser Asn Glu Leu Tyr Lys Val Gly Ala 305 310 315 320

Asn Val Lys Arg Lys Tyr Ser Ser Ala Glu Tyr Asn Asn Leu Asp Ile 325 330 335

Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Ala Leu Giy Asp Asp Val

Lys Tyr Phe Leu Ala Arg Leu Ile Gin Ala Phe Ala Pro Gly Ile Pro 355 360 365

Gin Val Tyr Tyr Val Giy Leu Leu Ala Giy Lys Asn Asp Leu Lys Leu 370 375 380

Leu Glu Glu Thr Lys Val Gly Arg Asn IIe Asn Arg His Tyr Tyr Ser 385 390 395 400

Asn Giu Giu ile Ala Giu Giu Val Gin Arg Pro Val Val Lys Ala Leu 405 410 415

Leu Asn Leu Phe Ser Phe Arg Asn Arg Ser Val Ala Phe Asp Leu Glu 420 430

Gly Thr lle Asp Val Glu Thr Pro Thr Ala His Ser Ile Val lle Lys 435 440 445

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		aca Thr														768
		gct Ala		Pro												816
		cga Arg 275	Leu													864

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lie Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Gly Thr Asn 195 200 205

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His Tyr Thr lle Pro Gln Lys lle Asn Ala His Gly Tyr Phe Thr Tyr 245 250 255

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Thr Asn Arg Leu Ala Asn Trp Leu Lys Gin Ser Pro Met Lys Gin Phe 275 280 285

Thr Thr Leu Asp Thr His Asp Gly 11e Gly Val Val Asp Ala Arg Asp 290 . 295 300

lle Leu Thr Asp Glu Glu lle Asp Tyr Ala Ser Glu Glu Leu Tyr Lys 305 310 315

Val Giy Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ala Tyr Asn Asn 325 330 335

Leu Asp ile Tyr Gin ile Asn Ser Thr Tyr Tyr Ser Ala Leu Giy Asn $340 \hspace{1.5cm} 345 \hspace{1.5cm} 350 \hspace{1.5cm}$

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Tyr Tyr Thr Arg Glu Glu Ite Lys Ser Ala Val Lys Arg Pro Val Val 405 415

Ala Asp Leu Leu Ala Leu Leu Ser Trp Arg Asn Gln Phe Ser Ala Phe 420 425 430

Ala Leu Asp Gly Thr lle Thr Val Glu Thr Pro Ser Glu His Asp lle

440

445

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(213) Lactobacillus acidophilus

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Lys Thr lie Gly Gly lie His Leu Leu Pro Phe Phe Pro Ser Asn Gly
35 40 45

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Asp Arg Gly Phe Ser Pro Thr Arg Tyr Asp Val Val Glu Pro Lys Phe
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Gly Ser Trp Glu Asp Val Glu Lys Leu Ser Gln Lys Tyr Tyr Leu Met
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Gin Met Asp Leu Asp Val Arg Thr Lys Thr Thr Gin Asp Phe lie Lys
165
170

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(213) Lactobacillus acidophilus

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672

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Tyr Gin lie Asn Thr Thr Tyr Tyr Ser Ala Leu Gly Asn Asp Asp Lys 340 345 350

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Gly Ser lle Glu 435		Pro Asn Glu As 440	sn Vai lle Gin 445	lie Thr
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Gin He Asp Leu	Asp Val Thr / 165	Ala Glu Val Th 170:	nr Lys Glu Phe	lle Arg 175
Gin Thr lie Lys	Asn Met Ala	Ala His Gly Cy 185	rs Ser lle Leu 190	

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Gin lie Tyr Tyr Val Gly Leu Leu Ala Gly Lys Asn Asp lie Asp Leu 370 375 380

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Cys Asn Leu Leu Arg Phe Arg Asn Thr Ser Glu Ala Phe Asp Leu Glu 420 425 430

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								Lys			acg Thr					624
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aaa Lys	tac Tyr	ttt Phe 355	ttg Leu	gcc Ala	cgc Arg	t t g Leu	ata IIe 360	caa GIn	gc t Ala	ttt Phe	gct Ala	cca Pro 365	ggt Gly	att	cca Pro	1104
cag GIn	gtt Val 370	tat Tyr	tac Tyr	gtt Val	ggc Gly	ttt Phe 375	tta Leu	gc t Ala	ggc Gly	aag Lys	aat Asn 380	gat Asp	ctt Leu	gaa Glu	t ta Leu	1152
											cgt Arg					1200
											gtt Val					1248
tta Leu	aat Asn	ctc Leu	ttt Phe 420	act Thr	tac Tyr	cgc Arg	aat Asn	cag Gin 425	tca Ser	gca Ala	gc t Ala	ttt Phe	gat Asp 430	ttg Leu	gat Asp	1296
											acc Thr					1344
											gca Ala 460					1392

caa gat atg aca tac aga gta aca gaa aat gat caa aca ata agc ttt Gln Asp Met Thr Tyr Arg Val Thr Glu Asn Asp Gln Thr Ile Ser Phe 465 470 475

gaa Glu 1440

1443

Artificial Sequence

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<400> 22

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Gly Lys Asn Leu Lys Glu Leu Asn Glu Asn Ile Glu Asn Tyr Phe Gly 20 25 30

Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Ser Gly 35 40 45

Asp Arg Gly Phe Ala Pro IIe Asp Tyr His Glu Val Asp Pro Ala Phe 50 55 60

Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys His Tyr Leu Met 65 70 75 80

Phe Asp Phe Met IIe Asn His IIe Ser Arg Gln Ser Lys Tyr Tyr Lys 85 90 95

Asp Tyr Gln Glu Lys His Glu Ala Ser Ala Tyr Lys Asp Leu Phe Leu 100 105 110

Asn Trp Asp Lys Phe Trp Pro Lys Asn Arg Pro Thr Gin Giu Asp Leu 115 120 125

Asp Leu lie Tyr Lys Arg Lys Asp Arg Ala Pro Met Gin Glu lie Arg 130 135 140

Phe Ala Asp Gly Ser Val Glu His Leu Trp Ser Thr Phe Gly Glu Glu 145 150 155 160

Gin ile Asp Leu Asp Val Thr Lys Giu Val Thr Met Asp Phe ile Arg 165 170 175

Ser Thr lie Glu Asn Leu Ala Ala Asn Gly Cys Asp Leu lie Arg Leu 180 185 190

Asp Ala Phe Ala Tyr Ala Val Lys Lys Leu Asp Thr Asn Asp Phe Phe 195 200 205

Val Glu Pro Glu lle Trp Thr Leu Leu Asp Lys Val Arg Asp lle Ala 210 215 220

Ala Val Ser Gly Ala Glu lle Leu Pro Glu lle His Glu His Tyr Thr 225 230 235 240

lle Gin Phe Lys lie Ala Asp His Gly Tyr Tyr Val Tyr Asp Phe Ala 245 250 255

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg 260 265 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly Ile Gly Val Val Asp Val Lys Asp Ile Leu Thr

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EG014US-Sequence Listing.txt
                                      Page 35
Asp Glu Glu lle Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala
305 310 315 320
Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp lle
325 330 335
Tyr Gin lie Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Gin 340 345
Lys Tyr Phe Leu Ala Arg Leu IIe Gin Ala Phe Ala Pro Giy IIe Pro 355 360 365
Gin Val Tyr Tyr Val Gly Phe Leu Ala Gly Lys Asn Asp Leu Glu Leu
370 375 380
Leu Giu Ser Thr Lys Giu Giy Arg Asn IIe Asn Arg His Tyr Tyr Ser
385 390 395 400
Ser Glu Glu IIe Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu
405 410 415
Leu Asn Leu Phe Thr Tyr Arg Asn Gin Ser Ala Ala Phe Asp Leu Asp 420 425 430
Gly Arg lie Glu Val Glu Thr Pro Asn Glu Ala Thr lie Val ile Glu 435 440 445
Arg Gin Asn Lys Asp Gly Ser His lie Ala Thr Ala Glu lle Asn Leu
450 455 460
Gin Asp Met Thr Tyr Arg Val Thr Giu Asn Asp Gin Thr Ile Ser Phe
465 470 475 480
Glu
        Artificial Sequence
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<221> CDS
<222> (1)..(1461)
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Met Pro lie Thr Asn Lys Thr Met Leu lie Thr Tyr Ala Asp Ser Leu
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96
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gat gct gtt ggc ggt gtc cat ttg ctg cca ttc ttt cct tcc aca ggt Asp Ala Val Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly 35 40 45

gat cgt ggc ttt gca ccg att gat tac cat gaa gtt gac tct gct ttt Asp Arg Gly Phe Ala Pro lle Asp Tyr His Glu Val Asp Ser Ala Phe 50 55 60

ggc gat tgg gat gat gtc aaa cgt ttg ggt gaa aaa tat tac ctc atg Gly Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met 65 70 75 80 144

240

											•						
EG0	14US	-Seq	uenc	e Li	stin	g. tx	t	Рa	ge 3	6							
t t t Phe	gat Asp	t t c Phe	atg Met	att Ile 85	aat Asn	cat His	att	tcg Ser	cgt Arg 90	cag Gln	tct Ser	aaa Lys	tat Tyr	tat Tyr 95	aaa Ly.s	288	
	tac Tyr													Phe		336	
	tgg Trp							Asn								384	
	ctg Leu 130															432	
	gca Ala															480	
cag Gin	att Ile	ga t Asp	ctt Leu	gac Asp 165	gtg Val	act Thr	aaa Lys	gaa Glu	gtg Val 170	act Thr	atg Met	gat Asp	ttt Phe	att 11e 175	cgc Arg	528	
	acc Thr															576	
ga t Asp	gcc Ala	ttt Phe 195	gc t Ala	tat Tyr	gct Ala	gtt Val	aaa Lys 200	aag Lys	c t a Leu	gat Asp	acg Thr	aat Asn 205	gat Asp	t t c Phe	ttt Phe	624	
	gaa Glu 210															672	
	gta Val															720	
	caa GIn															768	
	cct Pro															816	
	gcc Ala															864	
gat Asp	aca Thr 290	cat His	gac Asp	gg t Gly	att	ggt Gly 295	gtg Val	gtt Val	ga t Asp	gtt Val	aag Lys 300	gat Asp	atc	ctg Leu	ac t Thr	912	
	gaa Glu															960	
Asn	gtc Val	.As n	Arg	Lys 325	Tyr	Ser	Thr	Āla	Ğ1 u 330	Tyr	Asn	Asn	Leu	Asp 335	lle	1008	
	caa Gin															1056	
	tac Tyr															1104	
	gtt Val 370															1152	
Leu 385	gaa Glu	Ser	Thr	Lys	G1 u 390	Gly	Arg	Asn	lle	Asn 395	Arg	His	Туг	Tyr	Ser 400	1200	
agt Ser	gaa Glu	gaa Glu	att He	gct Ala 405	aag Lys	gaa Glu	gtg Val	aag Lys	cgg Arg 410	cca Pro	gtt Val	gtc Val	aag Lys	gca Ala 415	ctt Leu	1248	
tta	aat	ctc	ttt	ac t	tac	cgc	aat	cag	tca	gca	gct	ttt	gat	ttg	gat	1296	

EG014US-Sequence Li	sting.txt	Page 37	
Leu Asn Leu Phe Thr	Tyr Arg Asn	Gin Ser Ala Ala	Phe Asp Leu Asp
420		425	430
ggc cgt att gaa gtg Gly Arg lle Glu Val 435			
cgt caa aat aaa gat	ggc agt cat	atc gca aca gca	Glu ile Asn Leu
Arg Gln Asn Lys Asp	Gly Ser His	lle Ala Thr Ala	
450	455	460	
caa gat atg aca tac	aga gta aca	gaa aat gat caa	aca ata agc tta
GIn Asp Met Thr Tyr	Arg Vai Thr	Glu Asn Asp Gln	Thr IIe Ser Leu
465	470	475	480
tcc atg ata agc tgt Ser Met lie Ser Cys 485	Gin Thr		
<pre><210> 24 <211> 487 <212> PRT <213> Artificial S</pre>	equence		
<220> <223> Synthetic Co	nstruct		
<400> 24			
Met Pro Ile Thr Asn	Lys Thr Met	Leu lle Thr Tyr	Ala Asp Ser Leu
1 5		10	15
Gly Lys Asn Leu Lys	Glu Leu Asn	Glu Asn Ile Glu	Asn Tyr Phe Gly
20		25	30
Asp Ala Val Gly Gly	Val His Leu	Leu Pro Phe Phe	Pro Ser Thr Gly
35	40		45
Asp Arg Gly Phe Ala	Pro IIe Asp	Tyr His Glu Val	Asp Ser Ala Phe
50	55	60	
Gly Asp Trp Asp Asp	Val Lys Arg	Leu Gly Glu Lys	Tyr Tyr Leu Met
65	70	75	80
Phe Asp Phe Met Ile	Asn His IIe	Ser Arg GIn Ser	Lys Tyr Tyr Lys
85		90	95
Asp Tyr Gin Glu Lys	His Glu Ala	Ser Ala Tyr Lys	Asp Leu Phe Leu
100		105	110
Asn Trp Asp Lys Phe	Trp Pro Lys	Asn Arg Pro Thr	GIn Glu Asp Val
115	120		125
Asp Leu lle Tyr Lys	Arg Lys Asp	Arg Ala Pro Lys	Gin Glu ile Gin
130	135	140	
Phe Ala Asp Gly Ser	Val Glu His	Leu Trp Asn Thr	Phe Gly Glu Glu
145	150	155	160
Gin lie Asp Leu Asp		Glu Val Thr Met	Asp Phe IIe Arg
165		170	175
Ser Thr IIe Glu Asn	Leu Ala Ala	Asn Gly Cys Asp	Leu IIe Arg Leu
180		185	190
Asp Ala Phe Ala Tyr	Ala Val Lys	Lys Leu Asp Thr	Asn Asp Phe Phe
195	200		205
Val Glu Pro Glu Ile	Trp Thr Leu	Leu Asp Lys Val	Arg Asp lle Ala
210	215	220	

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Ala Val Ser Gly Ala Glu IIe Leu Pro Glu IIe His Glu His Tyr Thr 225 230 235 240

lle Gin Phe Lys Ile Ala Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala $245 \hspace{1.5cm} 250 \hspace{1.5cm} 255$

Leu Pro Met Val Thr Leu Tyr Ser Leu Tyr Ser Gly Lys Val Asp Arg 260 270

Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gin Phe Thr Thr Leu 275 280 285

Asp Thr His Asp Gly IIe Gly Val Val Asp Val Lys Asp IIe Leu Thr 290 295 300

Asp Glu Glu lle Thr Tyr Thr Ser Asn Glu Leu Tyr Lys Val Gly Ala 305 310 315 320

Asn Val Asn Arg Lys Tyr Ser Thr Ala Glu Tyr Asn Asn Leu Asp lle 325 330 335

Tyr Gin lle Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asp Asp Gin 340 350

Lys Tyr Phe Leu Ala Arg Leu IIe Gin Ala Phe Ala Pro Gly IIe Pro 355 360 365

Gin Vai Tyr Tyr Vai Gly Phe Leu Ala Gly Lys Asn Asp Leu Giu Leu 370 380

Leu Glu Ser Thr Lys Glu Gly Arg Asn IIe Asn Arg His Tyr Tyr Ser 385 390 395 400

Ser Glu Glu IIe Ala Lys Glu Val Lys Arg Pro Val Val Lys Ala Leu 405 410 415

Leu Asn Leu Phe Thr Tyr Arg Asn Gin Ser Ala Ala Phe Asp Leu Asp 420 430

Gly Arg Ile Glu Val Glu Thr Pro Asn Glu Ala Thr Ile Val Ile Glu 435 440 445

Arg Gin Asn Lys Asp Gly Ser His 11e Ala Thr Ala Glu 11e Asn Leu 450 460

Gin Asp Met Thr Tyr Arg Val Thr Giu Asn Asp Gin Thr lie Ser Leu 465 470 475 480

Ser Met Ile Ser Cys Gin Thr 485

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Arg Gly Phe Ala Pro IIe Asp Tyr His Glu Val Asp Ser Ala Phe Gly 20 25 30

Asp Trp Asp Asp Val Lys Arg Leu Gly Glu Lys Tyr Tyr Leu Met Phe

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35 40 45

Asp Phe Met IIe Asn His lie Ser 50

(210> 26
(211> 42
(212> PRT
(213> Streptococcus mutans)
(400> 26

Arg Pro Thr Gin Glu Asp Val Asp Leu lie Tyr Lys Arg Lys Asp Arg 10

Ala Pro Lys Gln Glu IIe Gin Phe Ala Asp Gly Ser Val Glu His Leu 20

Trp Asn Thr Phe Gly Glu Glu Gln IIe Asp 40

(210> 27
(211> 38
(212> PRT
(213> Streptococcus mutans)
(400> 27

Ile Leu Pro Glu IIe His Glu His Tyr Thr IIe Gln Phe Lys IIe Ala 10

Asp His Asp Tyr Tyr Val Tyr Asp Phe Ala Leu Pro Met Val Thr Leu 25
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Tyr Ser Leu Tyr Ser Gly 35